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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=4; day=4; hr=10; min=57; sec=23; ms=140;]

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Application No: 10588140 Version No: 2.0

Input Set:

Output Set:

Started: 2008-03-25 11:51:39.770
Finished: 2008-03-25 11:51:40.868
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 98 ms
Total Warnings: 9
Total Errors: 3
No. of SeqIDs Defined: 9
Actual SeqID Count: 9

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 257	Invalid sequence data feature in <221> in SEQ ID (8)
E 257	Invalid sequence data feature in <221> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 257	Invalid sequence data feature in <221> in SEQ ID (9)

SEQUENCE LISTING

<110> KIM, DO-MAN
KANG, HEE-KYOUNG
LEE, JIN-HA

<120> PROTEIN WITH ACTIVITY OF HYDROLYZING DEXTRAN, STARCH,
MUTAN, INULIN, AND LEVAN, GENE ENCODING THE SAME, CELL
EXPRESSING THE SAME, AND PRODUCTION METHOD THEREOF

<130> 44352-0010-00-US

<140> 10588140

<141> 2006-07-31

<150> PCT/KR05/00234

<151> 2005-01-27

<150> KR 10-2004-0006185

<151> 2004-01-30

<160> 9

<170> PatentIn Ver. 3.3

<210> 1

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
construct

<400> 1

Met Thr Leu Ile Tyr Val Pro Ser Ile Phe Thr Met Val Pro Ser Ile
1 5 10 15

Thr Arg Ile Val Leu Val Asn Ile Leu Leu Ala Thr Leu Val Leu Gly
20 25 30

Ala Ala Val Leu Pro Arg Asp Asn Arg Thr Val Cys Gly Ser Gln Leu
35 40 45

Cys Thr Trp Trp His Asp Ser Gly Glu Ile Asn Thr Gly Thr Pro Val
50 55 60

Gln Ala Gly Asn Val Arg Gln Ser Arg Lys Tyr Ser Val His Val Ser
65 70 75 80

Leu Ala Asp Arg Asn Gln Phe Tyr Asp Ser Phe Val Tyr Glu Ser Ile
85 90 95

Pro Arg Asn Gly Asn Gly Arg Ile Tyr Ser Pro Thr Asp Pro Pro Asn
100 105 110

Ser	Asn	Thr	Leu	Asn	Ser	Ser	Ile	Asp	Asp	Gly	Ile	Ser	Ile	Glu	Pro	115	120	125	
Ser	Leu	Gly	Ile	Asn	Met	Ala	Trp	Ser	Gln	Phe	Glu	Tyr	Arg	Arg	Asp	130	135	140	
Val	Asp	Ile	Lys	Ile	Thr	Thr	Ile	Asp	Gly	Ser	Ile	Leu	Asp	Gly	Pro	145	150	155	160
Leu	Asp	Ile	Val	Ile	Arg	Pro	Thr	Ser	Val	Lys	Tyr	Ser	Val	Lys	Arg	165	170	175	
Cys	Val	Gly	Gly	Ile	Ile	Ile	Arg	Val	Pro	Tyr	Asp	Pro	Asn	Gly	Arg	180	185	190	
Lys	Phe	Ser	Val	Glu	Leu	Lys	Ser	Asp	Leu	Tyr	Ser	Tyr	Leu	Ser	Asp	195	200	205	
Gly	Ser	Gln	Tyr	Val	Thr	Ser	Gly	Gly	Ser	Val	Val	Gly	Val	Glu	Pro	210	215	220	
Lys	Asn	Ala	Leu	Val	Ile	Phe	Ala	Ser	Pro	Phe	Leu	Pro	Arg	Asp	Met	225	230	235	240
Val	Pro	His	Met	Thr	Pro	His	Asp	Thr	Gln	Thr	Met	Lys	Pro	Gly	Pro	245	250	255	
Ile	Asn	Asn	Gly	Asp	Trp	Gly	Ser	Lys	Pro	Ile	Leu	Tyr	Phe	Pro	Pro	260	265	270	
Gly	Val	Tyr	Trp	Met	Asn	Glu	Asp	Thr	Ser	Gly	Asn	Pro	Gly	Lys	Leu	275	280	285	
Gly	Ser	Asn	His	Met	Arg	Leu	Asp	Pro	Asn	Thr	Tyr	Trp	Val	His	Leu	290	295	300	
Ala	Pro	Gly	Ala	Tyr	Val	Lys	Gly	Ala	Ile	Glu	Tyr	Phe	Thr	Lys	Gln	305	310	315	320
Asn	Phe	Tyr	Ala	Thr	Gly	His	Gly	Val	Leu	Ser	Gly	Glu	Asn	Tyr	Val	325	330	335	
Tyr	Gln	Ala	Asn	Ala	Ala	Asp	Asn	Tyr	Tyr	Ala	Val	Lys	Ser	Asp	Gly	340	345	350	
Thr	Ser	Leu	Arg	Met	Trp	Trp	His	Asn	Asn	Leu	Gly	Gly	Gly	Gln	Thr	355	360	365	
Trp	Phe	Cys	Met	Gly	Pro	Thr	Ile	Asn	Ala	Pro	Pro	Phe	Asn	Thr	Met	370	375	380	
Asp	Phe	Asn	Gly	Asn	Ser	Asn	Ile	Ser	Ser	Arg	Ile	Ser	Asp	Tyr	Lys	385	390	395	400
Gln	Val	Gly	Ala	Tyr	Phe	Phe	Gln	Thr	Asp	Gly	Pro	Glu	Ile	Tyr	Glu	405	410	415	

Asp Ser Val Val His Asp Val Phe Trp His Val Asn Asp Asp Ala Ile
 420 425 430
 Lys Thr Tyr Tyr Ser Gly Ala Ser Ile Ser Arg Ala Thr Ile Trp Lys
 435 440 445
 Cys His Asn Asp Pro Ile Ile Gln Met Gly Trp Thr Ser Arg Asn Leu
 450 455 460
 Thr Gly Ile Ser Ile Asp Asn Leu His Val Ile His Thr Arg Tyr Phe
 465 470 475 480
 Lys Ser Glu Thr Val Val Pro Ser Ala Ile Ile Gly Ala Ser Pro Phe
 485 490 495
 Tyr Ala Ser Gly Met Thr Val Asp Pro Ser Glu Ser Ile Ser Met Thr
 500 505 510
 Ile Ser Asn Val Val Cys Glu Gly Leu Cys Pro Ser Leu Phe Arg Ile
 515 520 525
 Thr Pro Leu Gln Ser Tyr Asn Asn Leu Val Val Lys Asn Val Ala Phe
 530 535 540
 Pro Asp Gly Leu Gln Thr Asn Pro Ile Gly Ile Gly Glu Ser Ile Ile
 545 550 555 560
 Pro Ala Ala Ser Gly Cys Thr Met Asp Leu Glu Ile Thr Asn Trp Thr
 565 570 575
 Val Lys Gly Gln Lys Val Thr Met Gln Asn Phe Gln Ser Gly Ser Leu
 580 585 590
 Gly Gln Phe Asp Ile Asp Gly Ser Tyr Trp Gly Gln Trp Ser Ile Asn
 595 600 605

<210> 2

<211> 2052

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic construct

<220>

<221> CDS

<222> (42)..(1865)

<400> 2

tggggtgtgtc ccttgctctg ccaacgttgt tgattgtttt c atg aca tta atc tac 56
 Met Thr Leu Ile Tyr
 1 5

gtg cct tca ata ttt aca atg gtc ccc tca atc aca cgg att gta ctg 104
 Val Pro Ser Ile Phe Thr Met Val Pro Ser Ile Thr Arg Ile Val Leu

10										15					20					
gtt aac att ctg ttg gcg acg ttg gtt ttg gga gct gca gtc ctt cca	152																			
Val Asn Ile Leu Leu Ala Thr Leu Val Leu Gly Ala Ala Val Leu Pro																				
25 30 35																				
cga gac aac aga act gtt tgc ggg agt caa ctc tgc aca tgg tgg cac	200																			
Arg Asp Asn Arg Thr Val Cys Gly Ser Gln Leu Cys Thr Trp Trp His																				
40 45 50																				
gac tcc ggc gag ata aac acc ggt act cct gta cag gca gga aac gtt	248																			
Asp Ser Gly Glu Ile Asn Thr Gly Thr Pro Val Gln Ala Gly Asn Val																				
55 60 65																				
cga caa tcc cga aag tac tct gtc cat gtg agc ctg gca gac cgt aac	296																			
Arg Gln Ser Arg Lys Tyr Ser Val His Val Ser Leu Ala Asp Arg Asn																				
70 75 80 85																				
caa ttc tac gac tct ttc gta tat gaa tcg ata cct agg aac ggc aat	344																			
Gln Phe Tyr Asp Ser Phe Val Tyr Glu Ser Ile Pro Arg Asn Gly Asn																				
90 95 100																				
ggc aga att tat tct ccc acc gac cca cct aac agc aat aca ttg aat	392																			
Gly Arg Ile Tyr Ser Pro Thr Asp Pro Pro Asn Ser Asn Thr Leu Asn																				
105 110 115																				
agt agc att gac gac ggt ata tca atc gaa cca tct ctc ggc atc aac	440																			
Ser Ser Ile Asp Asp Gly Ile Ser Ile Glu Pro Ser Leu Gly Ile Asn																				
120 125 130																				
atg gct tgg tcc cag ttc gaa tat aga cga gat gtc gac att aag att	488																			
Met Ala Trp Ser Gln Phe Glu Tyr Arg Arg Asp Val Asp Ile Lys Ile																				
135 140 145																				
act aca atc gat ggc tca ata ttg gat ggc cct ttg gac att gtt att	536																			
Thr Thr Ile Asp Gly Ser Ile Leu Asp Gly Pro Leu Asp Ile Val Ile																				
150 155 160 165																				
cgg ccg act tct gtt aag tac tca gtc aaa aga tgt gtg ggt ggt atc	584																			
Arg Pro Thr Ser Val Lys Tyr Ser Val Lys Arg Cys Val Gly Gly Ile																				
170 175 180																				
att att aga gtc cct tat gat ccc aat ggt cga aaa ttc tct gtt gag	632																			
Ile Ile Arg Val Pro Tyr Asp Pro Asn Gly Arg Lys Phe Ser Val Glu																				
185 190 195																				
tta aag agt gac ctt tac agt tac ctc tcc gac ggt tcg caa tat gtg	680																			
Leu Lys Ser Asp Leu Tyr Ser Tyr Leu Ser Asp Gly Ser Gln Tyr Val																				
200 205 210																				
acc tct gga ggg agc gtg gtt ggt gtg gag cca aaa aat gcc ctg gtg	728																			
Thr Ser Gly Gly Ser Val Val Gly Val Glu Pro Lys Asn Ala Leu Val																				
215 220 225																				
atc ttt gcc agc cct ttc ttg cca cgg gat atg gtt cct cat atg aca	776																			
Ile Phe Ala Ser Pro Phe Leu Pro Arg Asp Met Val Pro His Met Thr																				
230 235 240 245																				

cca cac gac acc cag aca atg aag ccg ggc cca atc aat aat ggg gac	824
Pro His Asp Thr Gln Thr Met Lys Pro Gly Pro Ile Asn Asn Gly Asp	
250 255 260	
tgg ggt tca aag cct ata ctc tac ttc ccg cct ggc gta tac tgg atg	872
Trp Gly Ser Lys Pro Ile Leu Tyr Phe Pro Pro Gly Val Tyr Trp Met	
265 270 275	
aac gag gat acc tct ggt aac ccc ggg aag ctc ggc tca aat cat atg	920
Asn Glu Asp Thr Ser Gly Asn Pro Gly Lys Leu Gly Ser Asn His Met	
280 285 290	
cgg ctg gat ccc aat acc tac tgg gtc cat cta gcc cca gga gcc tat	968
Arg Leu Asp Pro Asn Thr Tyr Trp Val His Leu Ala Pro Gly Ala Tyr	
295 300 305	
gtg aaa gga gcc att gag tat ttc acg aag caa aat ttc tat gca acg	1016
Val Lys Gly Ala Ile Glu Tyr Phe Thr Lys Gln Asn Phe Tyr Ala Thr	
310 315 320 325	
ggg cat ggc gtt ctc tca ggt gag aac tat gtt tat cag gcc aat gca	1064
Gly His Gly Val Leu Ser Gly Glu Asn Tyr Val Tyr Gln Ala Asn Ala	
330 335 340	
gct gat aac tac tat gcc gtc aag agt gat ggc aca agc ttg aga atg	1112
Ala Asp Asn Tyr Tyr Ala Val Lys Ser Asp Gly Thr Ser Leu Arg Met	
345 350 355	
tgg tgg cac aac aac ctt gga ggc ggt caa aca tgg ttt tgc atg ggg	1160
Trp Trp His Asn Asn Leu Gly Gly Gly Gln Thr Trp Phe Cys Met Gly	
360 365 370	
ccc acc att aat gca ccg ccg ttt aat acg atg gac ttc aac gga aac	1208
Pro Thr Ile Asn Ala Pro Pro Phe Asn Thr Met Asp Phe Asn Gly Asn	
375 380 385	
tct aat att tcc agc ccg att agt gac tat aag cag gtt ggc gct tat	1256
Ser Asn Ile Ser Ser Arg Ile Ser Asp Tyr Lys Gln Val Gly Ala Tyr	
390 395 400 405	
ttt ttc caa aca gac gga ccg gag atc tac gag gac agt gtt gtc cat	1304
Phe Phe Gln Thr Asp Gly Pro Glu Ile Tyr Glu Asp Ser Val Val His	
410 415 420	
gac gtc ttc tgg cat gtt aat gat gat gcc atc aag aca tat tat tcc	1352
Asp Val Phe Trp His Val Asn Asp Asp Ala Ile Lys Thr Tyr Tyr Ser	
425 430 435	
gga gct tca att tca cga gca acc atc tgg aag tgt cac aat gac ccg	1400
Gly Ala Ser Ile Ser Arg Ala Thr Ile Trp Lys Cys His Asn Asp Pro	
440 445 450	
atc ata cag atg ggc tgg acg tca cga aat ctc acc gga atc agc att	1448
Ile Ile Gln Met Gly Trp Thr Ser Arg Asn Leu Thr Gly Ile Ser Ile	
455 460 465	

gat aac ctg cac gtc atc cac acg aga tat ttc aaa tct gaa aca gtg 1496
 Asp Asn Leu His Val Ile His Thr Arg Tyr Phe Lys Ser Glu Thr Val
 470 475 480 485

gtt cct tca gca atc att gga gcg tct cca ttc tac gca agt gga atg 1544
 Val Pro Ser Ala Ile Ile Gly Ala Ser Pro Phe Tyr Ala Ser Gly Met
 490 495 500

act gtt gat ccc agc gag tcc atc agc atg acc atc tct aac gtg gtg 1592
 Thr Val Asp Pro Ser Glu Ser Ile Ser Met Thr Ile Ser Asn Val Val
 505 510 515

tgt gag ggt cta tgc ccc tca ctg ttc cgt atc act ccg ctt cag agc 1640
 Cys Glu Gly Leu Cys Pro Ser Leu Phe Arg Ile Thr Pro Leu Gln Ser
 520 525 530

tac aac aac ctt gtt gtc aag aac gtg gcc ttt ccc gat gga ctg cag 1688
 Tyr Asn Asn Leu Val Val Lys Asn Val Ala Phe Pro Asp Gly Leu Gln
 535 540 545

aca aat cca atc gga ata gga gag agc att ata cca gca gct tcc ggc 1736
 Thr Asn Pro Ile Gly Ile Gly Glu Ser Ile Ile Pro Ala Ala Ser Gly
 550 555 560 565

tgt aca atg gac ttg gaa atc aca aac tgg acc gtc aaa gga caa aaa 1784
 Cys Thr Met Asp Leu Glu Ile Thr Asn Trp Thr Val Lys Gly Gln Lys
 570 575 580

gtc acc atg caa aac ttt cag tcc ggg tca ctt ggc cag ttc gat atc 1832
 Val Thr Met Gln Asn Phe Gln Ser Gly Ser Leu Gly Gln Phe Asp Ile
 585 590 595

gat ggt tca tac tgg ggt caa tgg tcc ata aac taaagctatt ccattcacc 1885
 Asp Gly Ser Tyr Trp Gly Gln Trp Ser Ile Asn
 600 605

tgagtatttt cgtgggttca atgagttctt gttactgatg gggcccttgc tagtggtaaa 1945

agtagaggga cttgtcctcg ccgggcgcca aggaagttca tgtcttctag ttgaatagta 2005

tttgtttctt ctctctcgtt aaaaaaaaaa aaaaaaaaaa aaaaaaa 2052

<210> 3

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 3

gtcccttgag ctcccaac

18

<210> 4

<211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 4
 tcaactagaa ttcatagaact tcc 23

 <210> 5
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 5
 gagagagaga gagagagaga actagtctcg agtttttttt tttttttttt 50

 <210> 6
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 6
 acctggcaya grdmm 15

 <210> 7
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 7
 gsykccsacc tgcttrta 18

 <210> 8
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>

<223> Description of Artificial Sequence: Synthetic
peptide

<220>

<221> MOD_RES

<222> (5)

<223> Asp or Asn

<220>

<221> MOD_RES

<222> (6)

<223> Asn, Ser or Thr

<400> 8

Thr Trp Trp His Xaa Xaa

1 5

<210> 9

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<220>

<221> MOD_RES

<222> (6)

<223> Ser or Ala

<400> 9

Tyr Lys Gln Val Gly Xaa

1 5